Serial No. 09/538,396
Group Art Unit: 1638

A1

-- The present invention describes the maize Rad50 protein, which clearly possesses features characteristic of other Rad50 proteins, and has a calculated molecular weight of ~152.5 kDa. The maize Rad50 protein is characterized by the presence of an ATP binding site in the N-terminal region, a second nucleotide binding site in the C-terminal region, putative nuclear localization signals, and heptad-repeats. The presence of extensive leucine zipper structures appears to be another striking feature of the Rad50 proteins. These are also found in the maize Rad50 protein and are indicated in **bold** in Example 4. The present invention also describes a maize Rad50 polynucleotide sequence. The maize Rad50 orthologue of the present invention was used as a probe to map the maize RAD50 gene(s) to the short arm of chromosome 4. --

Please replace the paragraph beginning on page 17, line 9, with the following rewritten paragraph:

A2

-- Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold. These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is

used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915). --

Please replace the paragraph beginning on page 62, line 8, with the following rewritten paragraph:

-- Gene identities were determined by conducting BLAST (Basic Local Alignment Search Tool; Altschul, S. F., et al., (1990) J. Mol. Biol. 215:403-410) searches under default parameters for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm. The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish, W. and States, D. J. Nature Genetics 3:266-272 (1993)) provided by the NCBI. In some cases, the sequencing data from

Serial No. 09/538,396
Group Art Unit: 1638

A3 cont'd

two or more clones containing overlapping segments of DNA were used to construct contiguous DNA sequences. --

Please replace the Abstract beginning at page 67, line 1, with the following rewritten Abstract: